OIPE

ENTERED

RAW SEQUENCE LISTING   DATE: 04/29/2002
PATENT APPLICATION: US/10/040,416   TIME: 14:32:22

Input Set : A:\217969US0XCIP.txt
Output Set: N:\CRF3\04292002\J040416.raw

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 3 <110> APPLICANT: OOKURA, TETUYA
 4        KASUMI, TAKAFUMI
 5        ASABA, EIJI
 7 <120> TITLE OF INVENTION: ERYTHROSE REDUCTASE, ITS cDNA AND CELL WHICH THE cDNA
EXPRESS
 9 <130> FILE REFERENCE: 217969US0XCIP
11 <140> CURRENT APPLICATION NUMBER: 10/040,416
12 <141> CURRENT FILING DATE: 2002-01-09
14 <150> PRIOR APPLICATION NUMBER: US 09/800,487
15 <151> PRIOR FILING DATE: 2001-03-08
17 <150> PRIOR APPLICATION NUMBER: JP 2001-001294
18 <151> PRIOR FILING DATE: 2001-01-09
20 <160> NUMBER OF SEQ ID NOS: 10
22 <170> SOFTWARE: PatentIn version 3.1
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 1119
26 <212> TYPE: DNA
27 <213> ORGANISM: Trichosporonoides megachiliensis
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30 <221> NAME/KEY: CDS
31 <222> LOCATION: (1)..(993)
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38 1               5                  10                  15
40 gcc ctt gga ttt ggt act tgg caa gct gaa cct ggt caa gtg ggt gca        96
41 Ala Leu Gly Phe Gly Thr Trp Gln Ala Glu Pro Gly Gln Val Gly Ala
42               20                  25                  30
44 agt gtc aag aac gct gtc aag gct ggg tac cgt cat ttg gat ttg gcc       144
45 Ser Val Lys Asn Ala Val Lys Ala Gly Tyr Arg His Leu Asp Leu Ala
46           35                  40                  45
48 aaa gtg tac caa aac caa tcg gaa att gga gta gca ctt cag gaa ctg       192
49 Lys Val Tyr Gln Asn Gln Ser Glu Ile Gly Val Ala Leu Gln Glu Leu
50     50                  55                  60
52 ttt gat caa ggt att gtt aaa cgg gaa gat ttg ttt att acg tcc aaa       240
53 Phe Asp Gln Gly Ile Val Lys Arg Glu Asp Leu Phe Ile Thr Ser Lys
54 65                  70                  75                  80
56 gta tgg aat aac cgt cat gct cct gaa cat gtt gag cct gca ttg gac       288
57 Val Trp Asn Asn Arg His Ala Pro Glu His Val Glu Pro Ala Leu Asp
58               85                  90                  95
60 gaa aca ttg aaa gaa ctt gga ttg tcc tac ttg gat ttg tac ttg att       336
61 Glu Thr Leu Lys Glu Leu Gly Leu Ser Tyr Leu Asp Leu Tyr Leu Ile
62               100                 105                 110
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64  cat tgg ccc gtt gcg ttc aag ttt act acg cct caa gaa cta ttc cct      384
65  His Trp Pro Val Ala Phe Lys Phe Thr Thr Pro Gln Glu Leu Phe Pro
66          115             120             125
68  act gag ccg gat aac aag gaa ttg gcc gcg att gat gat tca atc aag      432
69  Thr Glu Pro Asp Asn Lys Glu Leu Ala Ala Ile Asp Asp Ser Ile Lys
70      130             135             140
72  ttg gta gac act tgg aag gca gtt gta gca ctc aaa aaa acg ggt aag      480
73  Leu Val Asp Thr Trp Lys Ala Val Val Ala Leu Lys Lys Thr Gly Lys
74  145             150             155             160
76  acc aaa tcc gtt ggt gtg tcg aac ttc act acg gat ttg gta gac ttg      528
77  Thr Lys Ser Val Gly Val Ser Asn Phe Thr Thr Asp Leu Val Asp Leu
78              165             170             175
80  gtt gaa aaa gcg tcg ggg gaa cga ccg gcg gtc aat cag att gaa gca      576
81  Val Glu Lys Ala Ser Gly Glu Arg Pro Ala Val Asn Gln Ile Glu Ala
82              180             185             190
84  cac cca ttg tta caa cag gat gaa ttg gtt gct cat cac aag agt aaa      624
85  His Pro Leu Leu Gln Gln Asp Glu Leu Val Ala His His Lys Ser Lys
86          195             200             205
88  aac att gtg att act gcg tac agt cct ttg gga aac aat gtg agt ggg      672
89  Asn Ile Val Ile Thr Ala Tyr Ser Pro Leu Gly Asn Asn Val Ser Gly
90      210             215             220
92  aaa cca cct ctg act caa aac cct ggg att gaa gca act gcg aaa cgg      720
93  Lys Pro Pro Leu Thr Gln Asn Pro Gly Ile Glu Ala Thr Ala Lys Arg
94  225             230             235             240
96  tta aat cat act cct gct gcg gtc ttg ctt gca tgg ggg att caa cgt      768
97  Leu Asn His Thr Pro Ala Ala Val Leu Leu Ala Trp Gly Ile Gln Arg
98              245             250             255
100 gga tac agt gta ttg gtc aag agt gtt aca cct tct cga att gag agc      816
101 Gly Tyr Ser Val Leu Val Lys Ser Val Thr Pro Ser Arg Ile Glu Ser
102             260             265             270
104 aat tat gat cag att acc ctt tct cct gaa gaa ttc cag aag gtt acg      864
105 Asn Tyr Asp Gln Ile Thr Leu Ser Pro Glu Glu Phe Gln Lys Val Thr
106         275             280             285
108 gat ttg atc aag gaa tat ggc gaa agt cgc aac aat att ccg ttg aat      912
109 Asp Leu Ile Lys Glu Tyr Gly Glu Ser Arg Asn Asn Ile Pro Leu Asn
110     290             295             300
112 tat aaa cct tca tgg ccc atc agt gtg ttt ggt aca tcg gat gaa gct      960
113 Tyr Lys Pro Ser Trp Pro Ile Ser Val Phe Gly Thr Ser Asp Glu Ala
114 305             310             315             320
116 aag gct act cat aag att aac acc aac ctt tga gttcagtttg ggaactattt     1013
117 Lys Ala Thr His Lys Ile Asn Thr Asn Leu
118             325             330
120 aaagctgctt gctggtcaca ttattgtcag tacctaccat gaagaattca atattatttt     1073
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126 <211> LENGTH: 330
127 <212> TYPE: PRT
128 <213> ORGANISM: Trichosporonoides megachiliensis
130 <400> SEQUENCE: 2
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137             20              25              30
140 Ser Val Lys Asn Ala Val Lys Ala Gly Tyr Arg His Leu Asp Leu Ala
141         35              40              45
144 Lys Val Tyr Gln Asn Gln Ser Glu Ile Gly Val Ala Leu Gln Glu Leu
145     50              55              60
148 Phe Asp Gln Gly Ile Val Lys Arg Glu Asp Leu Phe Ile Thr Ser Lys
149 65              70              75              80
152 Val Trp Asn Asn Arg His Ala Pro Glu His Val Glu Pro Ala Leu Asp
153             85              90              95
156 Glu Thr Leu Lys Glu Leu Gly Leu Ser Tyr Leu Asp Leu Tyr Leu Ile .
157         100             105             110
160 His Trp Pro Val Ala Phe Lys Phe Thr Thr Pro Gln Glu Leu Phe Pro
161         115             120             125
164 Thr Glu Pro Asp Asn Lys Glu Leu Ala Ala Ile Asp Asp Ser Ile Lys
165     130             135             140
168 Leu Val Asp Thr Trp Lys Ala Val Val Ala Leu Lys Lys Thr Gly Lys
169 145             150             155             160
172 Thr Lys Ser Val Gly Val Ser Asn Phe Thr Thr Asp Leu Val Asp Leu
173             165             170             175
176 Val Glu Lys Ala Ser Gly Glu Arg Pro Ala Val Asn Gln Ile Glu Ala
177             180             185             190
180 His Pro Leu Leu Gln Gln Asp Glu Leu Val Ala His His Lys Ser Lys
181         195             200             205
184 Asn Ile Val Ile Thr Ala Tyr Ser Pro Leu Gly Asn Asn Val Ser Gly
185     210             215             220
188 Lys Pro Pro Leu Thr Gln Asn Pro Gly Ile Glu Ala Thr Ala Lys Arg
189 225             230             235             240
192 Leu Asn His Thr Pro Ala Ala Val Leu Leu Ala Trp Gly Ile Gln Arg
193             245             250             255
196 Gly Tyr Ser Val Leu Val Lys Ser Val Thr Pro Ser Arg Ile Glu Ser
197             260             265             270
200 Asn Tyr Asp Gln Ile Thr Leu Ser Pro Glu Glu Phe Gln Lys Val Thr
201         275             280             285
204 Asp Leu Ile Lys Glu Tyr Gly Glu Ser Arg Asn Asn Ile Pro Leu Asn
205     290             295             300
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218 <212> TYPE: DNA
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221 <220> FEATURE:
222 <221> NAME/KEY: CDS
223 <222> LOCATION: (1)..(987)

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232 gct ctt ggg tac ggt acc tgg caa gca gaa cct ggt cag gtc ggt gaa      96
233 Ala Leu Gly Tyr Gly Thr Trp Gln Ala Glu Pro Gly Gln Val Gly Glu
234             20                  25                  30
236 ggt gtc aag ctc gct gtt aag gct ggc tac cgt cat ttg gac ttg gcc     144
237 Gly Val Lys Leu Ala Val Lys Ala Gly Tyr Arg His Leu Asp Leu Ala
238         35                  40                  45
240 aaa gta tac cag aac caa acc gag att ggc caa gct ctc aag gaa ctg     192
241 Lys Val Tyr Gln Asn Gln Thr Glu Ile Gly Gln Ala Leu Lys Glu Leu
242     50                  55                  60
244 ttt gat gag ggt gtt gtc aag cgt gag gac ctt ttc atc act tcc aag     240
245 Phe Asp Glu Gly Val Val Lys Arg Glu Asp Leu Phe Ile Thr Ser Lys
246 65                  70                  75                  80
248 ctt tgg aac aac cgc cac gct cct gag cac gtt gag cct gcg ctc gac     288
249 Leu Trp Asn Asn Arg His Ala Pro Glu His Val Glu Pro Ala Leu Asp
250                 85                  90                  95
252 gag act ctt aag gag ttg ggt cta tcc tat ttg gac ctg tac ttg att     336
253 Glu Thr Leu Lys Glu Leu Gly Leu Ser Tyr Leu Asp Leu Tyr Leu Ile
254                 100                 105                 110
256 cac tgg cct gtt gct ttc aag ttc act act ccc gat gaa ctg ctt cct     384
257 His Trp Pro Val Ala Phe Lys Phe Thr Thr Pro Asp Glu Leu Leu Pro
258             115                 120                 125
260 gct gac cct acc aac aag gac ctt gcc tac att gac gat tcg gtc aaa     432
261 Ala Asp Pro Thr Asn Lys Asp Leu Ala Tyr Ile Asp Asp Ser Val Lys
262     130                 135                 140
264 ttg tcc gac acc tgg aag gcg gtc gtc gcc ctg aaa aag acg ggt aag     480
265 Leu Ser Asp Thr Trp Lys Ala Val Val Ala Leu Lys Lys Thr Gly Lys
266 145                 150                 155                 160
268 acc aag tcg gtt ggt gtt tcg aac ttc agc act cgt ctg gtc gac ttg     528
269 Thr Lys Ser Val Gly Val Ser Asn Phe Ser Thr Arg Leu Val Asp Leu
270                 165                 170                 175
272 gtt gag gaa gct tcg ggc gaa cgt cct gcg gtt aac cag atc gaa gct     576
273 Val Glu Glu Ala Ser Gly Glu Arg Pro Ala Val Asn Gln Ile Glu Ala
274             180                 185                 190
276 cac ccc ttg ttg caa caa gac gag ttg gtt gct cac cat aag agc aag     624
277 His Pro Leu Leu Gln Gln Asp Glu Leu Val Ala His His Lys Ser Lys
278             195                 200                 205
280 aac att gtc atc act gct tac agt ccc ttg ggc aac aat gtc gct ggt     672
281 Asn Ile Val Ile Thr Ala Tyr Ser Pro Leu Gly Asn Asn Val Ala Gly
282     210                 215                 220
284 aaa cca cct ctg act gag aat ccc ggt att gtg gat gct gct aag cgt     720
285 Lys Pro Pro Leu Thr Glu Asn Pro Gly Ile Val Asp Ala Ala Lys Arg
286 225                 230                 235                 240
288 ctg aac cat act cct gct gct gtg ctc att gct tgg ggt att caa cgc     768
289 Leu Asn His Thr Pro Ala Ala Val Leu Ile Ala Trp Gly Ile Gln Arg
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              Input Set : A:\217969US0XCIP.txt
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290              245              250              255
292 ggg tac agc gtc ttg gtc aag tca gtt aca ccc tca cgg att aag agt     816
293 Gly Tyr Ser Val Leu Val Lys Ser Val Thr Pro Ser Arg Ile Lys Ser
294              260              265              270
296 aac ttt gaa cag atc act ctg tct gat gag gaa ttc caa cgg gtt acc     864
297 Asn Phe Glu Gln Ile Thr Leu Ser Asp Glu Glu Phe Gln Arg Val Thr
298              275              280              285
300 aac ctc atc aag gag tac ggt gag agc cgt aac aac gtt cct ttc aac     912
301 Asn Leu Ile Lys Glu Tyr Gly Glu Ser Arg Asn Asn Val Pro Phe Asn
302              290              295              300
304 tac aag cct tcg tgg tct att gac gtc ttt ggt acc cag tac gag gct     960
305 Tyr Lys Pro Ser Trp Ser Ile Asp Val Phe Gly Thr Gln Tyr Glu Ala
306 305              310              315              320
308 aag gct acc cac aag att aac gct taa tgtgctctta tacaaaaagt          1007
309 Lys Ala Thr His Lys Ile Asn Ala
310              325
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317 <210> SEQ ID NO: 4
318 <211> LENGTH: 328
319 <212> TYPE: PRT
320 <213> ORGANISM: Trichosporonoides megachiliensis
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329              20              25              30
332 Gly Val Lys Leu Ala Val Lys Ala Gly Tyr Arg His Leu Asp Leu Ala
333              35              40              45
336 Lys Val Tyr Gln Asn Gln Thr Glu Ile Gly Gln Ala Leu Lys Glu Leu
337              50              55              60
340 Phe Asp Glu Gly Val Val Lys Arg Glu Asp Leu Phe Ile Thr Ser Lys
341 65              70              75              80
344 Leu Trp Asn Asn Arg His Ala Pro Glu His Val Glu Pro Ala Leu Asp
345              85              90              95
348 Glu Thr Leu Lys Glu Leu Gly Leu Ser Tyr Leu Asp Leu Tyr Leu Ile
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352 His Trp Pro Val Ala Phe Lys Phe Thr Thr Pro Asp Glu Leu Leu Pro
353              115              120              125
356 Ala Asp Pro Thr Asn Lys Asp Leu Ala Tyr Ile Asp Asp Ser Val Lys
357              130              135              140
360 Leu Ser Asp Thr Trp Lys Ala Val Val Ala Leu Lys Lys Thr Gly Lys
361 145              150              155              160
364 Thr Lys Ser Val Gly Val Ser Asn Phe Ser Thr Arg Leu Val Asp Leu
365              165              170              175
368 Val Glu Glu Ala Ser Gly Glu Arg Pro Ala Val Asn Gln Ile Glu Ala
369              180              185              190
372 His Pro Leu Leu Gln Gln Asp Glu Leu Val Ala His His Lys Ser Lys
373              195              200              205
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 04/29/2002
PATENT APPLICATION: US/10/040,416   TIME: 14:32:23

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Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

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Seq#:8; N Pos. 3,9,18